

0300 T

BIOTECHNOLOGY SYSTEMS BRANCH

ASAY

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/543,679

Art Unit / Team No. :

O/PE

Date Processed by STIC:

4/25/2000

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/543,679

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
  
- 4      Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
  
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
  
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
  
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)                     . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
  
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      **(2) INFORMATION FOR SEQ ID NO:X:**  
                                 **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                                 **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
                                 **This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
  
- 9      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      **<210> sequence id number**  
                                 **<400> sequence id number**  
                                 **000**
  
- 10      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 11      Use of <213>Organism      Sequence(s)              are missing this mandatory field or its response.  
(NEW RULES)
  
- 12      Use of <220>Feature      Sequence(s)      are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
  
- 13      PatentIn ver. 2.0 "bug"      **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679

DATE: 04/25/2000  
TIME: 12:25:58

INPUT SET: S35381.raw

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

Does Not Comply  
Corrected Diskette Needed

SEQUENCE LISTING

1  
2  
3 (1) General Information  
4 (i) APPLICANT: East Carolina University  
5 et al.  
6 (ii) TITLE OF THE INVENTION: LOW ADENOSINE  
7 OLIGONUCLEOTIDE AGENT,  
8  
9 TREATMENTS  
10 (iii) NUMBER OF SEQUENCES: 3110  
11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: ARTER & HADDEN  
13 (B) STREET: 725 South Figueroa St, #  
14 3400  
15 (C) CITY: Los Angeles  
16 (D) STATE: CA  
17 (E) COUNTRY: USA  
18 (F) ZIP: 90071  
19 (v) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Diskette  
21 (B) COMPUTER: IBM Compatible  
22 (C) OPERATING SYSTEM: DOS  
23 (D) SOFTWARE: FastSEQ for Windows  
24 Version 2.0  
25 (vi) CURRENT APPLICATION DATA:  
26 (A) APPLICATION NUMBER: PCT/US99/  
27 (B) FILING DATE: 3-AUG-1999  
28 (C) CLASSIFICATION: UNKNOWN  
29 (vii) PRIOR APPLICATION DATA:  
30 (A) APPLICATION NUMBER: 60/095,212  
31 (B) FILING DATE: 03-AUG-1998  
32 (viii) ATTORNEY/AGENT INFORMATION:  
33 (A) NAME: Amzel, Viviana  
34 (B) REGISTRATION NUMBER: 30,930  
35 (C) REFERENCE/DOCKET NUMBER: EPI-109  
36 (ix) TELECOMMUNICATION INFORMATION:  
37 (A) TELEPHONE: 213-430-3520  
38 (B) TELEFAX: 213-617-9255  
39 (C) TELEX:  
40

*more up don't use TAB codes*

*FYI: all U.S. applications filed on or after July 1, 1998, and which do not claim a prior U.S. application or international application designating the United States, need to be in new Sequence Rules format*

ERRORED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:25:58

INPUT SET: S35381.raw

--> 41 (2) INFORMATION FOR SEQ ID NO:1:  
42 (i) SEQUENCE CHARACTERISTICS:  
43 (A) LENGTH: 21 base pairs  
44 (B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: single  
46 (D) TOPOLOGY: linear  
47 (ii) MOLECULE TYPE: cDNA  
48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
49 GATGGAGGGC GGCATGGCG G  
50 21  
51

*global  
format error  
→ 21*

--> 52 (2) INFORMATION FOR SEQ ID NO:2:  
53 (i) SEQUENCE CHARACTERISTICS:  
54 (A) LENGTH: 21 base pairs  
55 (B) TYPE: nucleic acid  
56 (C) STRANDEDNESS: single  
57 (D) TOPOLOGY: linear  
58 (ii) MOLECULE TYPE: cDNA  
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
60 GTAGCAGGCG GGGATGGGGG C  
61 21  
62

*same error*

--> 63 (2) INFORMATION FOR SEQ ID NO:3:  
64 (i) SEQUENCE CHARACTERISTICS:  
65 (A) LENGTH: 18 base pairs  
66 (B) TYPE: nucleic acid  
67 (C) STRANDEDNESS: single  
68 (D) TOPOLOGY: linear  
69 (ii) MOLECULE TYPE: cDNA  
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
71 GTTGTTGGGC ATCTTGCC  
72 18  
73

*same*

--> 74 (2) INFORMATION FOR SEQ ID NO:4:  
75 (i) SEQUENCE CHARACTERISTICS:  
76 (A) LENGTH: 18 base pairs  
77 (B) TYPE: nucleic acid  
78 (C) STRANDEDNESS: single  
79 (D) TOPOLOGY: linear  
80 (ii) MOLECULE TYPE: cDNA  
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
82 GTACTTGCGG ATCTAGGC  
83 18  
84

*same*

--> 85 (2) INFORMATION FOR SEQ ID NO:5:  
86 (i) SEQUENCE CHARACTERISTICS:  
87 (A) LENGTH: 18 base pairs  
88 (B) TYPE: nucleic acid  
89 (C) STRANDEDNESS: single

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:25:59

INPUT SET: S35381.raw

90 (D) TOPOLOGY: linear  
91 (ii) MOLECULE TYPE: cDNA  
92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
93 GTGGGCCTAG CTCTCGCC  
94 18  
95

--> 96 (2) INFORMATION FOR SEQ ID NO:6:  
97 (i) SEQUENCE CHARACTERISTICS:  
98 (A) LENGTH: 18 base pairs  
99 (B) TYPE: nucleic acid  
100 (C) STRANDEDNESS: single  
101 (D) TOPOLOGY: linear  
102 (ii) MOLECULE TYPE: cDNA  
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
104 GTCGGGGTAC CTGTCCGC  
105 18  
106

--> 107 (2) INFORMATION FOR SEQ ID NO:7:  
108 (i) SEQUENCE CHARACTERISTICS:  
109 (A) LENGTH: 21 base pairs  
110 (B) TYPE: nucleic acid  
111 (C) STRANDEDNESS: single  
112 (D) TOPOLOGY: linear  
113 (ii) MOLECULE TYPE: cDNA  
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
115 CTCGTCGCCG TCGCCGGCGG G  
116 21  
117

--> 118 (2) INFORMATION FOR SEQ ID NO:8:  
119 (i) SEQUENCE CHARACTERISTICS:  
120 (A) LENGTH: 20 base pairs  
121 (B) TYPE: nucleic acid  
122 (C) STRANDEDNESS: single  
123 (D) TOPOLOGY: linear  
124 (ii) MOLECULE TYPE: cDNA  
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
126 GGGTGGTGCT ATTGTCGGGC  
127 20  
128

--> 129 (2) INFORMATION FOR SEQ ID NO:9:  
130 (i) SEQUENCE CHARACTERISTICS:  
131 (A) LENGTH: 15 base pairs  
132 (B) TYPE: nucleic acid  
133 (C) STRANDEDNESS: single  
134 (D) TOPOLOGY: linear  
135 (ii) MOLECULE TYPE: cDNA  
136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
137 GGCCAGGGC CAGCC  
138 15

*same**✓*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:25:59

INPUT SET: S35381.raw

139

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140 (2) INFORMATION FOR SEQ ID NO:10:  
141 (i) SEQUENCE CHARACTERISTICS:  
--> 142 (A) LENGTH: 21 base pairs  
143 (B) TYPE: nucleic acid  
144 (C) STRANDEDNESS: single  
145 (D) TOPOLOGY: linear  
146 (ii) MOLECULE TYPE: cDNA  
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
148 GGCCGGGCCA GCCGGGCCG G  
149 21  
150

---

151 (2) INFORMATION FOR SEQ ID NO:11:  
152 (i) SEQUENCE CHARACTERISTICS:  
--> 153 (A) LENGTH: 50 base pairs  
154 (B) TYPE: nucleic acid  
155 (C) STRANDEDNESS: single  
156 (D) TOPOLOGY: linear  
157 (ii) MOLECULE TYPE: cDNA  
158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
159 GCGGCCTGGA AAGCTGAGAT GGAGGGCGGC ATGGCGGGCA CAGGCTGGGC  
160 50  
161

---

162 (2) INFORMATION FOR SEQ ID NO:12:  
163 (i) SEQUENCE CHARACTERISTICS:  
--> 164 (A) LENGTH: 49 base pairs  
165 (B) TYPE: nucleic acid  
166 (C) STRANDEDNESS: single  
167 (D) TOPOLOGY: linear  
168 (ii) MOLECULE TYPE: cDNA  
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
170 CGGCCTGGAA AGCTGAGATG GAGGGCGGCA TGGCGGGCAC AGGCTGGGC  
171 49  
172

---

173 (2) INFORMATION FOR SEQ ID NO:13:  
174 (i) SEQUENCE CHARACTERISTICS:  
--> 175 (A) LENGTH: 48 base pairs  
176 (B) TYPE: nucleic acid  
177 (C) STRANDEDNESS: single  
178 (D) TOPOLOGY: linear  
179 (ii) MOLECULE TYPE: cDNA  
180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
181 GGCCTGGAAG GCTGAGATGG AGGGCGGCAT GGCGGGCACA GGCTGGGC  
182 48  
183

---

184 (2) INFORMATION FOR SEQ ID NO:14:  
185 (i) SEQUENCE CHARACTERISTICS:  
--> 186 (A) LENGTH: 47 base pairs

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:25:59

INPUT SET: S35381.raw

187 (B) TYPE: nucleic acid  
188 (C) STRANDEDNESS: single  
189 (D) TOPOLOGY: linear  
190 (ii) MOLECULE TYPE: cDNA  
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
192 GCCTGGAAAAG CTGAGATGGA GGGCGGCATG GCGGGCACAG GCTGGGC  
193 47  
194

*Same*

--> 195 (2) INFORMATION FOR SEQ ID NO:15:  
196 (i) SEQUENCE CHARACTERISTICS:  
197 (A) LENGTH: 46 base pairs  
198 (B) TYPE: nucleic acid  
199 (C) STRANDEDNESS: single  
200 (D) TOPOLOGY: linear  
201 (ii) MOLECULE TYPE: cDNA  
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
203 CCTGGAAAAGC TGAGATGGAG GCGGCATGG CGGGCACAGG CTGGGC  
204 46  
205

--> 206 (2) INFORMATION FOR SEQ ID NO:16:  
207 (i) SEQUENCE CHARACTERISTICS:  
208 (A) LENGTH: 45 base pairs  
209 (B) TYPE: nucleic acid  
210 (C) STRANDEDNESS: single  
211 (D) TOPOLOGY: linear  
212 (ii) MOLECULE TYPE: cDNA  
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
214 CTGGAAAAGCT GAGATGGAGG GCGGCATGGC GGCACAGGC TGGGC  
215 45  
216

--> 217 (2) INFORMATION FOR SEQ ID NO:17:  
218 (i) SEQUENCE CHARACTERISTICS:  
219 (A) LENGTH: 44 base pairs  
220 (B) TYPE: nucleic acid  
221 (C) STRANDEDNESS: single  
222 (D) TOPOLOGY: linear  
223 (ii) MOLECULE TYPE: cDNA  
224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
225 TGGAAAGCTG AGATGGAGGG CCGCATGGCG GGCACAGGCT GGGC  
226 44  
227

--> 228 (2) INFORMATION FOR SEQ ID NO:18:  
229 (i) SEQUENCE CHARACTERISTICS:  
230 (A) LENGTH: 43 base pairs  
231 (B) TYPE: nucleic acid  
232 (C) STRANDEDNESS: single  
233 (D) TOPOLOGY: linear  
234 (ii) MOLECULE TYPE: cDNA  
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

*These errors  
are global. See  
item 1 on  
Error Summary  
sheet*

INPUT SET: S35381.raw

26157 8  
26158

26159 (2) INFORMATION FOR SEQ ID NO:2420:  
26160 (i) SEQUENCE CHARACTERISTICS:  
--> 26161 (A) LENGTH: 981 base pairs  
26162 (B) TYPE: nucleic acid  
26163 (C) STRANDEDNESS: single  
26164 (D) TOPOLOGY: linear  
26165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:  
26166 1 ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT  
26167 GCTCATGGCC  
26168 61 CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA  
26169 CCAGGCGCTG  
26170 121 CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC  
26171 CGTGGGTGGC  
26172 181 CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT  
26173 CCACACCTGG  
26174 241 CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC  
26175 CCTGCTGGCA  
26176 301 ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT  
26177 GGTGGTGACC  
26178 361 CCCCCGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT  
26179 GGTGGGACTG  
26180 421 ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC  
26181 AGCCAAAGGC  
26182 481 AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT  
26183 GGAGTACATG  
26184 541 GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT  
26185 CCTCATCTAC  
26186 601 CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC  
26187 CTCTTCGGC  
26188 661 GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC  
26189 CCTCATCTCT  
26190 721 TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC  
26191 CCTCTCTTGC  
26192 781 CCGTCTTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCTCAC  
26193 GCACGGCAAC  
26194 841 TCGGCCATGA ACCCATTTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT  
26195 CACCTTCCTT  
26196 901 AAGATTTGGA ATGACCATTT CCGTGCCAG CCTGCACCTC CCATTGACGA  
26197 GGATCTCCCA  
26198 961 GAAGAGAGGC CTGATGACTA G  
26199

? what format  
is  
this?  
60  
120

Cumulative  
base totals,  
per sequence  
Runs, need  
to be at  
right margin  
of each line

26200 (2) INFORMATION FOR SEQ ID NO:2421:  
26201 (i) SEQUENCE CHARACTERISTICS:  
--> 26202 (A) LENGTH: 2900 base pairs  
26203 (B) TYPE: nucleic acid  
26204 (C) STRANDEDNESS: single  
26205 (D) TOPOLOGY: linear  
26206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:  
26207 1 ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT



RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:29:08

INPUT SET: S35381.raw

26208 CTCCTCTGT  
26209 61 GAGGCTGGCA GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA  
26210 GCTAGCGGCT  
26211 121 GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC  
26212 GGGAGCTCTG  
26213 181 CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CCGGAGCCGG  
26214 AGGACTATGA  
26215 241 GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG CGCGGCCCGG  
26216 AGCTCTGTTC  
26217 301 CCTGGAACCT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG  
26218 ATGGTGCTTG  
26219 361 CCTCGTGCCC CTTGGTGCCC GTCTGCTGAT GTGCCCAGCC TGTGCCCCGC  
26220 ATGCCGCCCT  
26221 421 CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC  
26222 CTGGTCTCTG  
26223 481 TGCCCGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG  
26224 CGGGATGCCA  
26225 541 CCTTCTGCTT CATCGTGTG CTGGCGGTGG CTGATGTGGC CGTGGGTGCC  
26226 CTGGTCATCC  
26227 601 CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC  
26228 CTCATGGTTG  
26229 661 CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA  
26230 ATTGCTGTGG  
26231 721 ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC  
26232 CCCCCGAGGG  
26233 781 CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG  
26234 ACCCCTATGT  
26235 841 TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC  
26236 AGCATGGGGG  
26237 901 AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG  
26238 GTCTACTTCA  
26239 961 ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC  
26240 CTGGAGGTCT  
26241 1021 TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC  
26242 GACCCGCAGA  
26243 1081 AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCCTC  
26244 TTCCTCTTTG  
26245 1141 CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC  
26246 CCGTCCTGCC  
26247 1201 ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC  
26248 TCGGCCATGA  
26249 1261 ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT CACCTTCCTT  
26250 AAGATTTGGA  
26251 1321 ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA  
26252 GAAGAGAGGC  
26253 1381 CTGATGACTA GACCCCGCCT TCCGCTCCCA CCAGCCCACA TCCAGTGGGG  
26254 TCTCAGTCCA  
26255 1441 GTCCTCACAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG  
26256 GGCTGTTGGC  
26257 1501 TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC  
26258 CACTAGGAGT  
26259 1561 TAACTACCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT  
26260 CCTACGGAGG

*Same  
enum*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:29:08

INPUT SET: S35381.raw

26261 1621 GACCAGGTGT CTAGAGGCAA CAGTGTCTG AGCCCCCACC TGCCTGACCA  
26262 TCCCATGAGC  
26263 1681 AGTCCAGCGC TTCAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTGCAGA  
26264 GGAGCCACCT  
26265 1741 GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT  
26266 TGTCTTAGAT  
26267 1801 GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT  
26268 CTGAGACGGA  
26269 1861 TGGAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG  
26270 GCCAGAGGCA  
26271 1921 GCTAAGGGGC AGGAATCAAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG  
26272 GACCCCAGGC  
26273 1981 CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA  
26274 TTGTACGTGG  
26275 2041 GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG  
26276 TGCTGGCTCC  
26277 2101 ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA  
26278 CGAGGTGGTA  
26279 2161 GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT  
26280 GTAATTACCT  
26281 2221 GTCATCTGGG CCACCAGCTC CACTGGCCCC CGTTGCCGGG CCTGGACTGT  
26282 CCTAGGTGAC  
26283 2281 CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACA CTAGACATGC  
26284 CAACTCGGGA  
26285 2341 GCATTCTGCC TGCCTGGGAA CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC  
26286 TCAGTGTGTA  
26287 2401 CTGTAGGCGC CCCTGGGGTG GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG  
26288 AGTACCCCCC  
26289 2461 TGAGAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC  
26290 CTAGTATCTG  
26291 2521 GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT  
26292 AGGACTTTAG  
26293 2581 GGATCTGGGA TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC  
26294 CCCTGTGTTG  
26295 2641 GGGGGCAAGG TGGGGGAGCC TGGAGCCCCCT GTGTGGGAGG GCGAGGCGGG  
26296 GGAGCCTGGA  
26297 2701 GCCCCTGTGT GGGAGGGCGA GCGGGGGGAT CCTGGAGCCC CTGTGTCGGG  
26298 GGGCGAGGGA  
26299 2761 GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTC AACTCCAGGA  
26300 CTTGCTTCCA  
26301 2821 AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC  
26302 CCATGTGACT  
26303 2881 AATAAAAAAC TGTGAACCCCT  
26304

*done*

26305 (2) INFORMATION FOR SEQ ID NO:2422:  
26306 (i) SEQUENCE CHARACTERISTICS:  
--> 26307 (A) LENGTH: 1942 base pairs  
26308 (B) TYPE: nucleic acid  
26309 (C) STRANDEDNESS: single  
26310 (D) TOPOLOGY: linear  
26311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:  
26312 1 CGCATTTGTG TTTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG

*done*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:29:09

INPUT SET: S35381.raw

26313 AGACAAAGGA  
26314 61 AGGAAAATTT AAATCCTTAG ATTCAAGCAG AAGAAATCCA TGTGGAAGGT  
26315 TTGGGTGTGTT  
26316 121 GTTGTGTGTTG TTTGGTGTGT TTTTGTGTTT TTTGTTTTTT TGTTTTTTTTT  
26317 TGAGATGGAG  
26318 181 TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC  
26319 AGCCAGCTAC  
26320 241 CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG  
26321 AGCTAGCGGC  
26322 301 TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACA GTCAGGCAGC  
26323 CGGGAGCTCT  
26324 361 GCCAGCTTTG GTGACCTTGG GTGCTTGCCT CGTGCCCCCTT GGTGCCCCGTC  
26325 TGCTGATGTG  
26326 421 CCCAGCCTGT GCCCGCCATG CCGCCCCCCA TCTCAGCTTT CCAGGCCGCC  
26327 TACATCGGCA  
26328 481 TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGTATC  
26329 TGGGCGGTGA  
26330 541 AGGTGAACCA GCGCTGCGG GATGCCACCT TCTGCTTCAT CGTGTGCTG  
26331 GCGGTGCGTG  
26332 601 ATGTGGCCGT GGGTGCCCTG GTCATCCCCC TCGCCATCCT CATCAACATT  
26333 GGGCCACAGA  
26334 661 CCTACTTCCA CACCTGCCTC ATGGTTGCCT GTCCGGTCCT CATCCTCACC  
26335 CAGAGCTCCA  
26336 721 TCCTGGCCCT GCTGGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC  
26337 CCTCTCCGGT  
26338 781 ACAAGATGGT GGTGACCCCC CGGAGGGCGG CGGTGGCCAT AGCCGGCTGC  
26339 TGGATCCTCT  
26340 841 CCTTCGTGGT GGGACTGACC CCTATGTTTG GCTGGAACAA TCTGAGTGCG  
26341 GTGGAGCGGG  
26342 901 CCTGGGCAGC CAACGGCAGC ATGGGGGAGC CCGTGATCAA GTGCGAGTTC  
26343 GAGAAGGTCA  
26344 961 TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCCC  
26345 CCGCTTCTCC  
26346 1021 TCATGGTCCT CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC  
26347 AACAAGAAGG  
26348 1081 TGTCGGCCTC CTCCGGCGAC CCGCAGAAGT ACTATGGGAA GGAGCTGAAG  
26349 ATCGCCAAGT  
26350 1141 CGCTGGCCCT CATCCTCTTC CTCTTTGCCC TCAGCTGGCT GCCTTTGCAC  
26351 ATCCTCAACT  
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26353 ATTGCCATCT  
26354 1261 TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCCTTCCGC  
26355 ATCCAGAAGT  
26356 1321 TCCGCGTCAC CTTCTTAAG ATTTGGAATG ACCATTTCCG CTGCCAGCCT  
26357 GCACCTCCCA  
26358 1381 TTGACGAGGA TCTCCAGAA GAGAGGCCTG ATGACTAGAC CCCGCCTTCC  
26359 GCTCCCACCG  
26360 1441 CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC GCTGTCCCAG  
26361 GGGTCTCCCT  
26362 1501 GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGGG AGGCTCTGAA  
26363 GAGATACCA  
26364 1561 CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC  
26365 TGCAGGAGGC

*Done*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:29:09

INPUT SET: S35381.raw

26366 1621 CTGGGAGGGC AAGGGTCCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT  
26367 GTTCTGAGCC  
26368 1681 CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA  
26369 GGTCCCTGGGG  
26370 1741 AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT  
26371 TCTGCGGTGA  
26372 1801 GGCAGGGGAG TCTGCTTGTC TTAGATGTTG GTGGTGCAGC CCCAGGACCA  
26373 AGCTTAAGGA  
26374 1861 GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC  
26375 ACTGGCCTGT  
26376 1921 TCTGTAGGAG AGACTGGCCA GA  
26377

*Please correct this type of error  
in subsequent sequence?*

--> 26380 (2) INFORMATION FOR SEQ ID NO:2423:  
26379 (i) SEQUENCE CHARACTERISTICS:  
26381 (A) LENGTH: 5904 base pairs  
26382 (B) TYPE: nucleic acid  
26383 (C) STRANDEDNESS: single  
26384 (D) TOPOLOGY: linear  
26385 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:  
26385 ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC  
26386 CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA  
26387 CCAGGCGCTG CGGGATGCCA CCTTCTGCTT ATCGTCTCG CTGGCGGTGG CTGATGTGGC  
26388 CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT  
26389 CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC  
26390 CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT  
26391 GGTGGTGACC CCCCAGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT  
26392 GGTGGGACTG CCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC  
26393 AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT  
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26395 CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTGGC  
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26397 CCTCATCTCT TTCCTCTTTG CCCTCAGCTG GCTGCCCTTG CACATCCTCA ACTGCATCAC  
26398 CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC  
26399 GCACGGCAAC TCGGCCATGA ACCCATTTGT CTATGCCTTC CGCATCCAGA AGTTCCGCGT  
26400 CACCTTCCTT AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA  
26401 GGATCTCCCA GAAGAGAGGC CTGATGACTA G ATGAGTGTC GAAGTGTGAA  
26402 GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCCTCTGT GAGGCTGGCA GGTGAGGAAG  
26403 GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT GCTGAAGGCG TCGAGGTGTG  
26404 GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG  
26405 CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG AGGACTATGA GCTGCCGCGC GTTGTCCAGA  
26406 GCCCAGCCCA GCCCTACGCG CGCGGCCCGG AGCTCTGTTT CCTGGAACCT TGGGCACTGC  
26407 CTCTGGGACC CCTGCCGGCC AGCAGGCAGG ATGGTGCTTG CCTCGTGCCC CTGGGTGCC  
26408 GTCTGCTGAT GTGCCCAGCC TGTGCCCGCC ATGCCGCCCT CCATCTCAGC TTTCCAGGCC  
26409 GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGCTGGTG  
26410 ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTG  
26411 CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC  
26412 ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC  
26413 ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG  
26414 ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCAGAGGG CGGCGGTGGC CATAGCCGGC  
26415 TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT  
26416 GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGGCAG  
26417 TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG

*where  
are  
cumulative  
base totals?*

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:29:09

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26418 CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG  
26419 CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG  
26420 AAGATCGCCA AGTCGCTGGC CCTCATCCTC TTCTCTTTTG CCCTCAGCTG GCTGCCTTTG  
26421 CACATCCTCA ACTGCATCAC CCTCTTCTGC CCGTCCTGCC ACAAGCCCAG CATCCTTACC  
26422 TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC  
26423 CGCATCCAGA AGTTCCGCGT CACCTTCCTT AAGATTTGGA ATGACCATT TCCGCTGCCAG  
26424 CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA GACCCCGCCT  
26425 TCCGCTCCCA CCAGCCCACA TCCAGTGGGG TCTCAGTCCA GTCCTCACAT GCCCCGCTGTC  
26426 CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG GGCTGTTGGC TGGGGGCATG GGGGAGGCTC  
26427 TGAAGAGATA CCCACAGAGT GTGGTCCCTC CACTAGGAGT TAACTACCTT ACACCTCTGG  
26428 GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT CCTACGGAGG GACCAGGTGT CTAGAGGCAA  
26429 CAGTGTTCCT AGCCCCCACC TGCCCTGACCA TCCCATGAGC AGTCCAGCGC TTCAGGGCTG  
26430 GGCAGGTCTT GGGGAGGCTG AGACTGCAGA GGAGCCACCT GGGCTGGGAG AAGGTGCTTG  
26431 GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT GTTGGTGGTG CAGCCCCAGG  
26432 ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAGGAGA GAGGTTGAGG  
26433 ATGCACTGGC CTGTTCTGTA GGAGAGACTG GCCAGAGGCA GCTAAGGGGC AGGAATCAAG  
26434 GAGCCTCCGT TCCCACCTCT GAGGACTCTG GACCCAGGC CATAACAGGT GCTAGGGTGC  
26435 CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA TTGTACGTGG GAGAGGCAGA AAGGGTAGGT  
26436 TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC ACGCCCTGGG GAGTGAGCTT  
26437 GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC CTCCTTCTTG  
26438 CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT GTAATTACCT GTCATCTGGG CCACCAGCTC  
26439 CACTGGCCCC CGTTGCCGGG CCTGGACTGT CCTAGGTGAC CCCATCTCTG CTGCTTCTGG  
26440 GCCTGATGGA GAGGAGAACA CTAGACATGC CAACTCGGGA GCATTCTGCC TGCCCTGGGAA  
26441 CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC TCAGTGTTGA CTGTAGGCGC CCCTGGGGTG  
26442 GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG AGTACCCCC TGAGAGCATG TGGGGGAAGG  
26443 CCTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG GCTGGGTTTT CAGGGGCTTT  
26444 GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT AGGACTTTAG GGATCTGGGA TCTGGGGAAG  
26445 GACCAACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTTG GGGGGCAAGG TGGGGGAGCC  
26446 TGGAGCCCCT GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA GCCCCTGTGT GGGAGGGCGA  
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26450 CGCATTTGTG TTTTAATAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG AGACAAAGGA  
26451 AGGAAAATTT AAATCCTTAG ATTCAAGCAG AAGAATTCCA TGTGGAAGGT TTGGGTTGTT  
26452 GTTGTGTTTG TTTGGTGTGT TTTTGTGTTT TTTGTTTTTT TGTTTTTTTT TGAGATGGAG  
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26454 CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG AGCTAGCGGC  
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26456 GCCAGCTTTG GTGACCTTGG GTGCTTGCC TCGTCCCCCT GGTGCCCCGTC TGCTGATGTG  
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26458 TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGATC TGGGCGGTGA  
26459 AGGTGAACCA GGCCTGCGG GATGCCACCT TCTGCTTCAT CGTGTGCTG GCGGTGGCTG  
26460 ATGTGGCCGT GGGTGCCCTG GTCATCCCC TCGCCATCCT CATCAACATT GGGCCACAGA  
26461 CCTACTTCCA CACCTGCCTC ATGGTTGCCT GTCCGGTCCT CATCCTCACC CAGAGCTCCA  
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26463 ACAAGATGGT GGTGACCCCC CGGAGGGCGG CGGTGGCCAT AGCCGGCTGC TGGATCCTCT  
26464 CCTTCGTGGT GGGACTGACC CCTATGTTTG GCTGGAACAA TCTGAGTGCG GTGGAGCGGG  
26465 CCTGGGCAGC CAACGGCAGC ATGGGGGAGC CCGTGATCAA GTGCGAGTTC GAGAAGGTCA  
26466 TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCC  
26467 CCGCTTCTCC TCATGGTCCT CATCTACCTG GAGGTCTTCT ACCTAATCCG  
26468 CAAGCAGCTC AACAAGAAGG TGCTGGCCTC CTCCGGCGAC CCGCAGAAGT ACTATGGGAA  
26469 GGAGTGAAAG ATCGCCAAGT GCCTGCCCTT CATCCTCTTC CTCTTTGCC TCAGCTGGCT  
26470 GCCTTTGCAC ATCCTCAACT GCATCACCTT CTTCTGCCCC TCCTGCCACA AGCCCAGCAT

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PATENT APPLICATION US/09/543,679DATE: 04/25/2000  
TIME: 12:29:10

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26471 CCTTACCTAC ATTGCCATCT TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA  
26472 TGCCTTCCGC ATCCAGAAGT TCCGCGTCAC CTTCCCTAAG ATTTGGAATG ACCATTTCGG  
26473 CTGCCAGCCT GCACCTCCCA TTGACGAGGA TCTCCCAGAA GAGAGGCTG ATGACTAGAC  
26474 CCCGCCCTTC GCTCCCACCG CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCCC  
26475 GCTGTCCCAG GGGTCTCCCT GAGCCTGCCC CAGCTGGGCT GTTGGCTGGG GGCATGGGGG  
26476 AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC  
26477 CTCTGGGCCC TGCAGGAGGC CTGGGAGGGC AAGGGTCCTA CGGAGGGACC AGGTGTCTAG  
26478 AGGCAACAGT GTTCTGAGCC CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA  
26479 GGGCTGGGCA GGTCTTGGGG AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG  
26480 TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTTGTC TTAGATGTTG GTGGTGCAGC  
26481 CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG  
26482 TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA GAT GGA GGG CGG  
26483 CAT GGC GGG G CGG GTC GCT GG GGC GGG CBC BGG C GGC GGG CBC GC GGC  
26484 CTG G GGB GGG GGG C GBT GGB GGG GG CTG GGC GC GGC CTG GAA AGC  
26485 TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC  
26486

*same*  
*Please*  
*correct this*  
*type of error*  
*in*  
*subsequent*  
*sequences*

--> 26487 (2) INFORMATION FOR SEQ ID NO:2424:  
26488 (i) SEQUENCE CHARACTERISTICS:  
26489 (A) LENGTH: 1687 base pairs  
26490 (B) TYPE: nucleic acid  
26491 (C) STRANDEDNESS: single  
26492 (D) TOPOLOGY: linear  
26493 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:  
26494 1 CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT CCGGGCGCTA  
26495 TGGCCATGCC  
26496 61 CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GCGCGCCTT CGGTAGGGGG  
26497 CGCCCCGGGGC  
26498 121 CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC  
26499 GCTGGAGCTG  
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26510 481 TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCCT  
26511 TGCCTTTGGC  
26512 541 ATCGGATTGA CTCCATTCCCT GGGGTGGAAC AGTAAAGACA GTGCCACCAA  
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26514 601 GAACCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT  
26515 CTTTGAGAAT  
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26517 GCCCCCACTG  
26518 721 CTTATAATGC TGGTGATCTA CATTAAGATC TTCTGGTGG CCTGCAGGCA  
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26520 781 ACTGAGCTGA TGGACCACTC GAGGACCACC CTCCAGCGGG AGATCCATGC  
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26522 841 CTGGCCATGA TTGTGGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC